

AMSH1  
AMSH2  
AMSH  
Rpn11  
Jab1

THNE FTITHVIVP-- KQSAGPDYCDMENVEKLENVQDQHD-- LITLGWIEHPTQTAFLS  
THNE FTITHVIVP-- KQSAGPDYCDMENVEKLENVQDQHD-- LITLGWIEHPTQTAFLS  
MNE FTITHVILP-- KQSAGSDYCNTKEEELFLIQDQG-- LITLGWIEHPTQTAFLS  
TVRVIDVYAMQPS-- GTGVSVLAVD PVIQAXMIDMLXQTG RPEMVGVYHESPGIGCNLS  
TMIIMDSJALPVIGTEIRVNABQAAAYEYHAYIENAXQVGRLENAGHYSHPGIGCNLS

AMSH1  
AMSH2  
AMSH  
Rpn11  
Jab1

SVBLIHTICSYQMLPESVAIVCSPKHKDTG---- TIRLTNAGHLEVSACKKGFH-- PH  
SVBLIHTICSYQMLPESVAIVCSPKHKDTG---- TIRLTNAGHLEVSACKKGFH-- PH  
SVBLIHTICSYQMLPESVAIVCSPKHKDTG---- PTKITDNGILKRISSCRQKGFH-- PH  
GVIINTQQSFALSLERAVAVVVDPIQSVKGVVVIDAFRLINAMMVLGHKPROITSNLGH  
GIVSVSTQMLNQQJQTPIVAVVVIDPTRTISAG---- KVNLGAFRTYPRGYKPPDEGPSTYQ

AMSH1  
AMSH2  
AMSH  
Rpn11  
Jab1

TKEPRLFSICKHV-- LVKDIKI---- IVLDLR  
TKEPRLFSIQKFLSGIISGTAL---- EKXPLKIGYGPNGFPLLGISRS8SP8EQ  
SKDPPPLFCSCSHVT-- VVDRAV-- TITDLR  
LNKPB IQALIHGLNRHYYSITINYRKNELEQKMLLNHKKSMMEGLTQDYSEHCKHNES  
TIPLNKIEDFGVHCKQYYALEVSYFKSSLDRLKLELDRNQKYVNTLSSS3LLINADYTG

AMSH1  
AMSH2  
AMSH  
Rpn11  
Jab1

-----  
L-----  
VVKEMILELAKNYQIKAVKEDKMTFEQLAIKNVGRQDPRRHLKTHVDVLMTSNIVQCLAMM  
QVFDLSEKILEQSEAQLGRGSFMIG-- LETHDRKSUKLAKATRDSCKTIEATHGLMSQV

AMSH1  
AMSH2  
AMSH  
Rpn11  
Jab1

-----  
-----  
-----  
LDTVYVFK--  
IKDKLFLQJINIS

FIGURE 1

AMSH1	-----	MPDHTDVSLSPEERVRALSKLGCHITISEDITPRR	35
AMSH2	-----	MQPFITVNSLKKLJAAMPDHTDVSLSPEERVRALSKLGCHITISEDITPRR	50
AMSH	-----	MSDRGDVS LPPEDRVRALSKLGCHITISEDITPRR	35
	*****	*****	*****
AMSH1	YFRSGVEMERMASVYLEE	GNLEN A FVLYNK ITTLFVEK LPNHRDYQQCAV	85
AMSH2	YFRSGVEMERMASVYLEE	GNLEN A FVLYNK ITTLFVEK LPNHRDYQQCAV	100
AMSH	YFRSGVEMERMASVYLEE	GNLEN A FVLYNK ITTLFVEK LPNHRDYQQCAV	85
	*****	*****	*****
AMSH1	PEKQDIPMKLKEIAFPRTDEKLNDL	KK YNVEYQTYLQSKNKKKAEI	135
AMSH2	PEKQDIPMKLKEIAFPRTDEKLNDL	KK YNVEYQTYLQSKNKKKAEI	130
AMSH	PEKQDIPMKLKEIAFPRTDEKLNDL	KK YNVEYQTYLQSKNKKKAEI	135
	*****	*****	*****
AMSH1	LEHQRLIEAERKRIAQMRQQQLE	SEQFLITFEDQ LKKQE LARGQMRSSQTS	185
AMSH2	LEHQRLIEAERKRIAQMRQQQLE	SEQFLITFEDQ LKKQE LARGQMRSSQTS	200
AMSH	MAIQQELEKEKQRVADQKQOQLE	QEQFHAEYEMIRNQE LERERLKIVQEF	185
	*****	*****	*****
AMSH1	G-LSEQIDGSALS	CFS--THQNSLLNVFADQPNKSDATNYASHSPPVNR	232
AMSH2	G-LSEQIDGSALS	CFS--THQNSLLNVFADQPNKSDATNYASHSPPVNR	247
AMSH	GVVDPGIGOPLPDLEKPSLDVFTLTIVSSIQPSDCETTVRPAKPPVDR	235	
	*****	*****	*****
AMSH1	ALTPAATLSAVON	LVEGLRCVVLPEDLCHKFLQLAISNTVRGIETCGIL	282
AMSH2	ALTPAATLSAVON	LVEGLRCVVLPEDLCHKFLQLAISNTVRGIETCGIL	297
AMSH	SLKPGALSNSESI	PTIDGLRHVVVPGRLCPQJQLQLASANTARGVETCGIL	285
	*****	*****	*****
AMSH1	CGKLTHNE	FTITHVIVPKQSAGPDYCDHENVEE	332
AMSH2	CGKLTHNE	FTITHVIVPKQSAGPDYCDHENVEE	347
AMSH	CGKLTHNE	FTITHVIVPKQSAGPDYCDHENVEE	335
	*****	*****	*****
AMSH1	THPTOTAF	LSSVBLHTC SYQLMLPEAIAIVCSPKHDITGJFRINAGML	382
AMSH2	THPTOTAF	LSSVBLHTC SYQLMLPEAIAIVCSPKHDITGJFRINAGML	397
AMSH	THPTOTAF	LSSVBLHTC SYQLMLPEAIAIVCSPKHDITGJFRINAGML	385
	*****	*****	*****
AMSH1	EVSACKKG	GIPHHTIKEPRLFSICKHV	421
AMSH2	EVSACKKG	GIPHHTIKEPRLFSICKHV	447
AMSH	KISSCRQKG	GHFHSKDPPPLFCSCSHVT	424
	*****	*****	*****
AMSH1	-----	LLGISRSSSPSEQL	461
AMSH2	-----		
AMSH	-----		

FIGURE 2

COP9_sus5_Hs	VGRLENAIGWYHSHPGYGCWLSGIDVSTQMLNQQFQEPFVA--VVIDPRTTISAGKVNLG
COP9_sus5_Dm	VGRMEHAVGWHSHPGYGCWLSGINVSTQMLNQTYQEPFVA--IVVDPVRTVSAGKVCLG
COP9_sus5_At	AGRLENVVGWHSHPGYGCWLSGIDVSTQRLNQQHQEPFLA--VVIDPRTTVSAGKVEIG
COP9_sus5_Ce	EGRKEKVVGWHSHPGYGCWLSGIDVSTQTLNQKFQEPFWA--IVIDPLRTMSAGKVD1G
AF2198_Arcfu	LPIGMKVFGTVHSHPSCRPSEEDLSLFTFRGKYHIIIVCY--PYDENSWKCYNRKCEEV
PH0451_Pyrho	MPHDESIKGTFHSHPSPFYPSEGDLMFFSKFGGIHIIIAAF--PYDEDSVKAFCDSSEGREV
TVN1035_Thevo	KPIDFSLVGSVHSHPSGITKPSDEDLRMSLTSKGKIHIIIVGY--PYNLKDYSAYDRSGNKV
MTH971_Metht	LPPFTGAVGSVHSHPGPVNLPSSAADLHFFSLSKGFLFHIIIAH--PYTMETVAAVYTRNGDPV
aq_1691_Aquae	ISKGMEIVGVYHSHPDHPDRPSQFDLQRAPFDLSYIIIFSVQ--KGKVASYRSWELKGDKF
RV1334_Myctu	EDADEVPVVIYHSHTATEAPSRTDVKIMATEPDAYHVLUSTRDPRHRLERSYRIVDGAVT
RadC_Ecoli	I KINASALILAHNHPSGCAEPSKADKLITERIIKSCQFMDL--RVLDHIVIGRGEYVSFA
.....	.....HSHP'.....S 'D

**FIGURE 3**

COP9\_su5\_Hs VGRLENAIGWYHSHPGYGCWLSGIDVSTQMLNQQFQEPFVA--VVIDPTRTISAGKVNLG  
COP9\_su5\_Dm VGRMETHAVGWYHSHPGYGCWLSGINVSTQMLNQTYQEPFVA--VVVDPVRTVSAGKVCLG  
COP9\_su5\_At AGRLENVGWYHSHPGYGCWLSGIDVSTQRLNQQHQEPFLA--VVIDPTRTVSAGKVBIG  
COP9\_su5\_Ce EGRKEKVVGVWYHSHPGYGCWLSGIDVSTQTLNOKFOEPWVA--VVIDPLRTMSAGKVDIG  
Pad1\_Dm TGRPEMVGWYHSHPGFGCWLSGVDINTQQSFEALSERAVA--VVVDPPIQSVKG-KVVID  
Pad1\_Hs TGRPEMVGWYHSHPGFGCWLSGVDINTQQSFEALSERAVA--VVVDPPIQSVKG-KVVID  
Sks1\_Dd TGRDEIVIGWYHSHPGFGCWLSVDVNTQQSFEQLQSRAVA--VVVDPPLQSVRG-KVVID  
Pad1\_Sc TGRDOMVGWYHSHPGFGCWLSVDVNTQKSFEQLNSRAVA--VVVDPPIQSVKG-KVVID  
..... HSHP.....S 'D

FIGURE 4